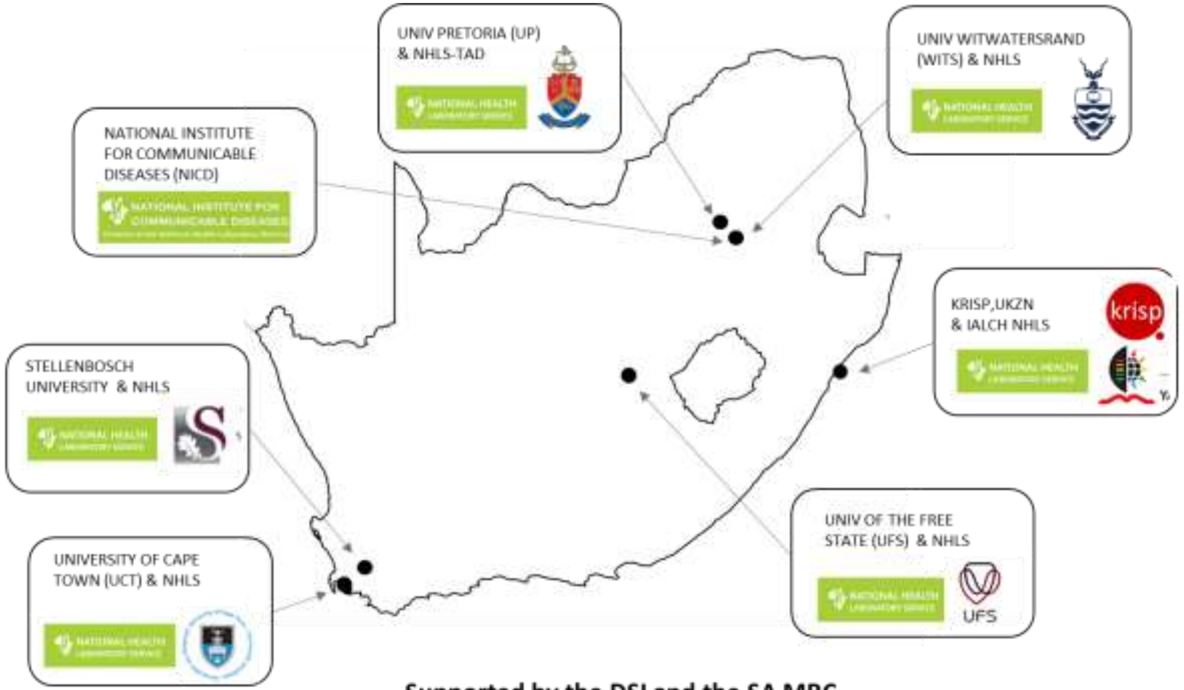
NGS-SA Network for Genomic Surveillance in South Africa

# Network for Genomic Surveillance in South Africa (NGS-SA)

# SARS-CoV-2 Sequencing Update

## 03 March 2023



UNIV PRETORIA (UP) & NHLS-TAD

UNIV WITWATERSRAND (WITS) & NHLS

NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES (NICD)

KRISP,UKZN & IALCH NHLS

STELLENBOSCH UNIVERSITY & NHLS

UNIV OF THE FREE STATE (UFS) & NHLS

UNIVERSITY OF CAPE TOWN (UCT) & NHLS

**Supported by the DSI and the SA MRC**

Msomi N. Mlisana K. et al. Lancet Microbe 2020

Prepared by the National Institute for Communicable Diseases (NICD) of the National Health Laboratory (NHLS) on behalf of the Network for Genomics Surveillance in South Africa (NGS-SA)

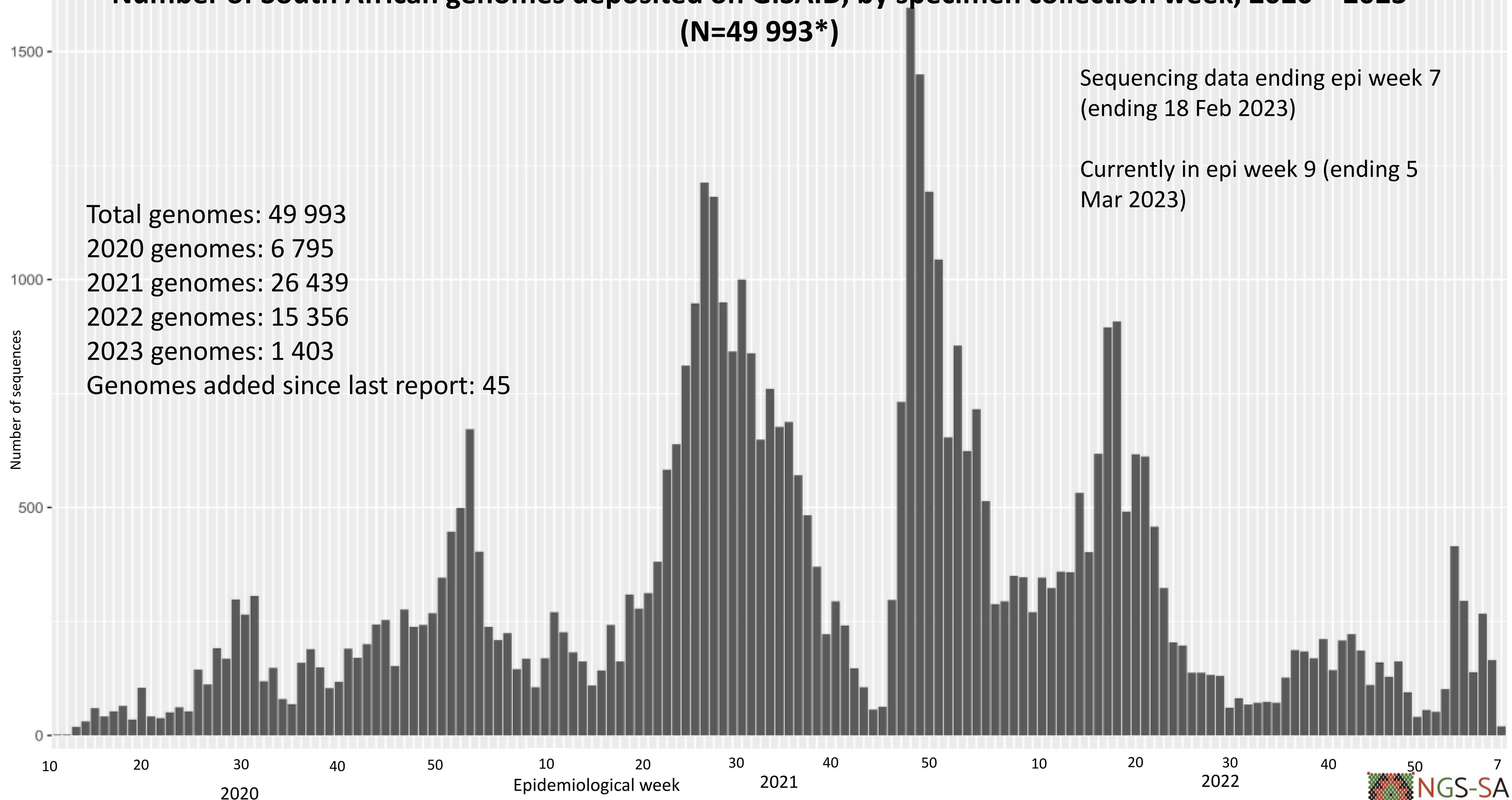
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 03 March 2023 at 09h00

Data license: https://www.gisaid.org/registration/terms-of-use/

Elbe, S., and Buckland-Merrett, G. (2017) Data, disease and diplomacy: GISAID's innovative contribution to global health. Global Challenges, 1:33-46. DOI: 10.1002/gch2.1018 PMCID: 31565258

Shu, Y., McCauley, J. (2017) GISAID: Global initiative on sharing all influenza data – from vision to reality. EuroSurveillance, 22(13) DOI: 10.2807/1560-7917.ES.2017.22.13.30494 PMCID: PMC5388101

# Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2023 (N=49 993*)



Sequencing data ending epi week 7 (ending 18 Feb 2023)

Currently in epi week 9 (ending 5 Mar 2023)

Total genomes: 49 993
2020 genomes: 6 795
2021 genomes: 26 439
2022 genomes: 15 356
2023 genomes: 1 403
Genomes added since last report: 45

*This represents the cleaned, de-duplicated dataset of unique **National and Pneumonia Surveillance** sequences. This dataset will be used for all further figures.

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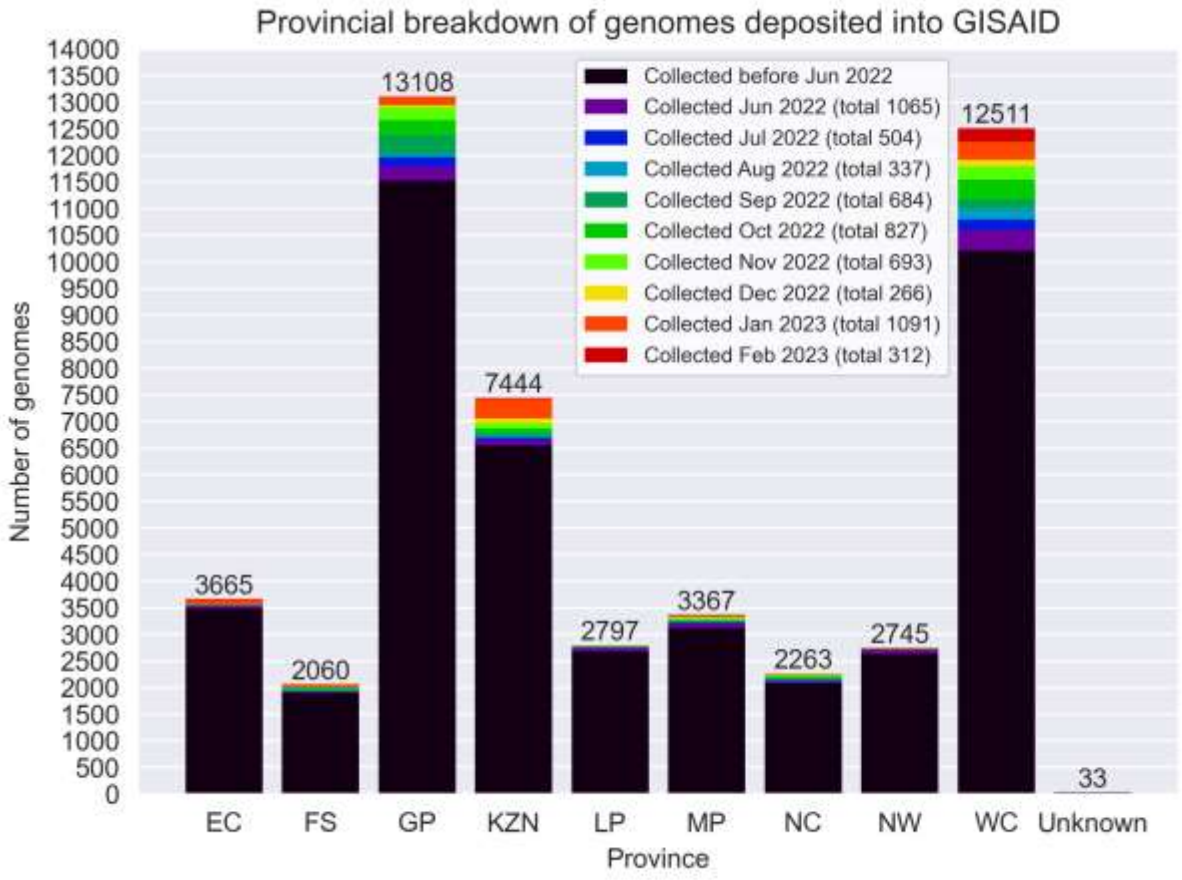
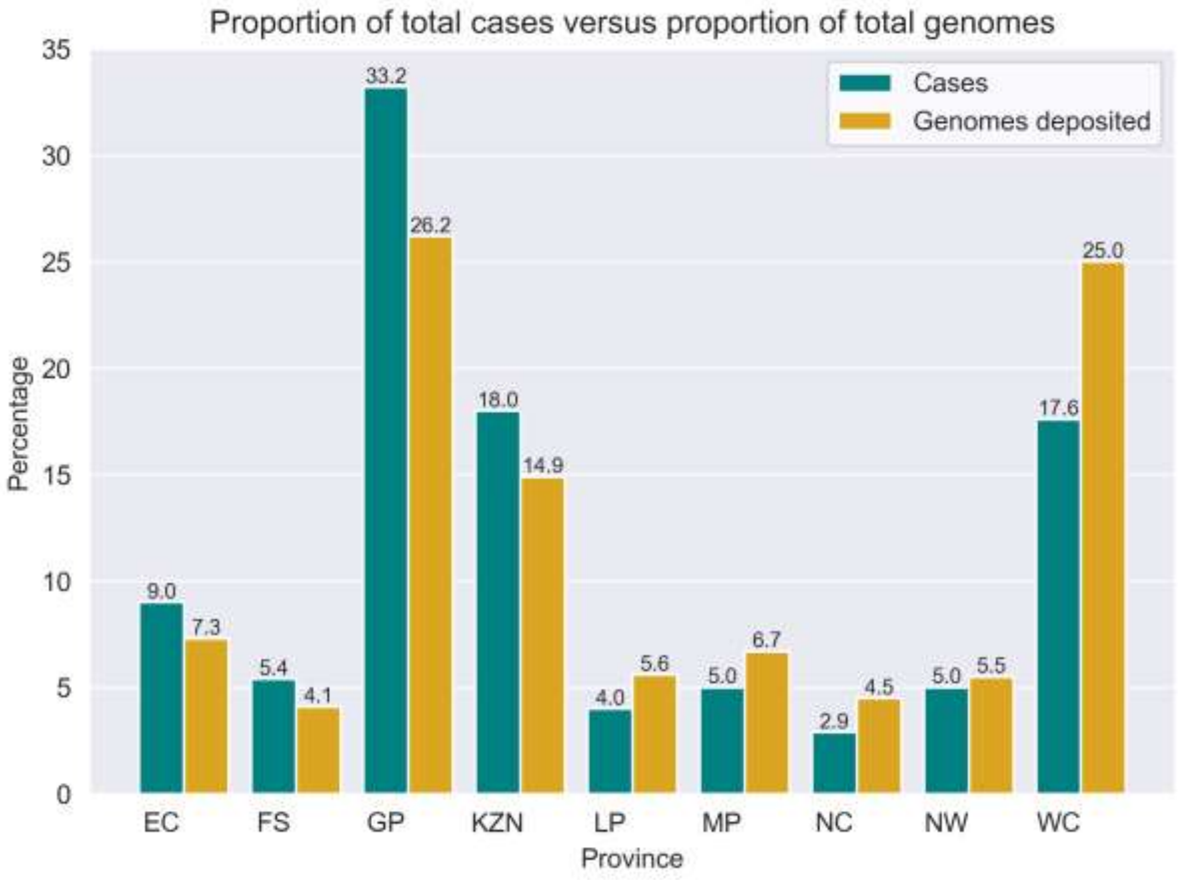
# GISAID genomes vs total cases, 2020 – 2023 (N=49 993)





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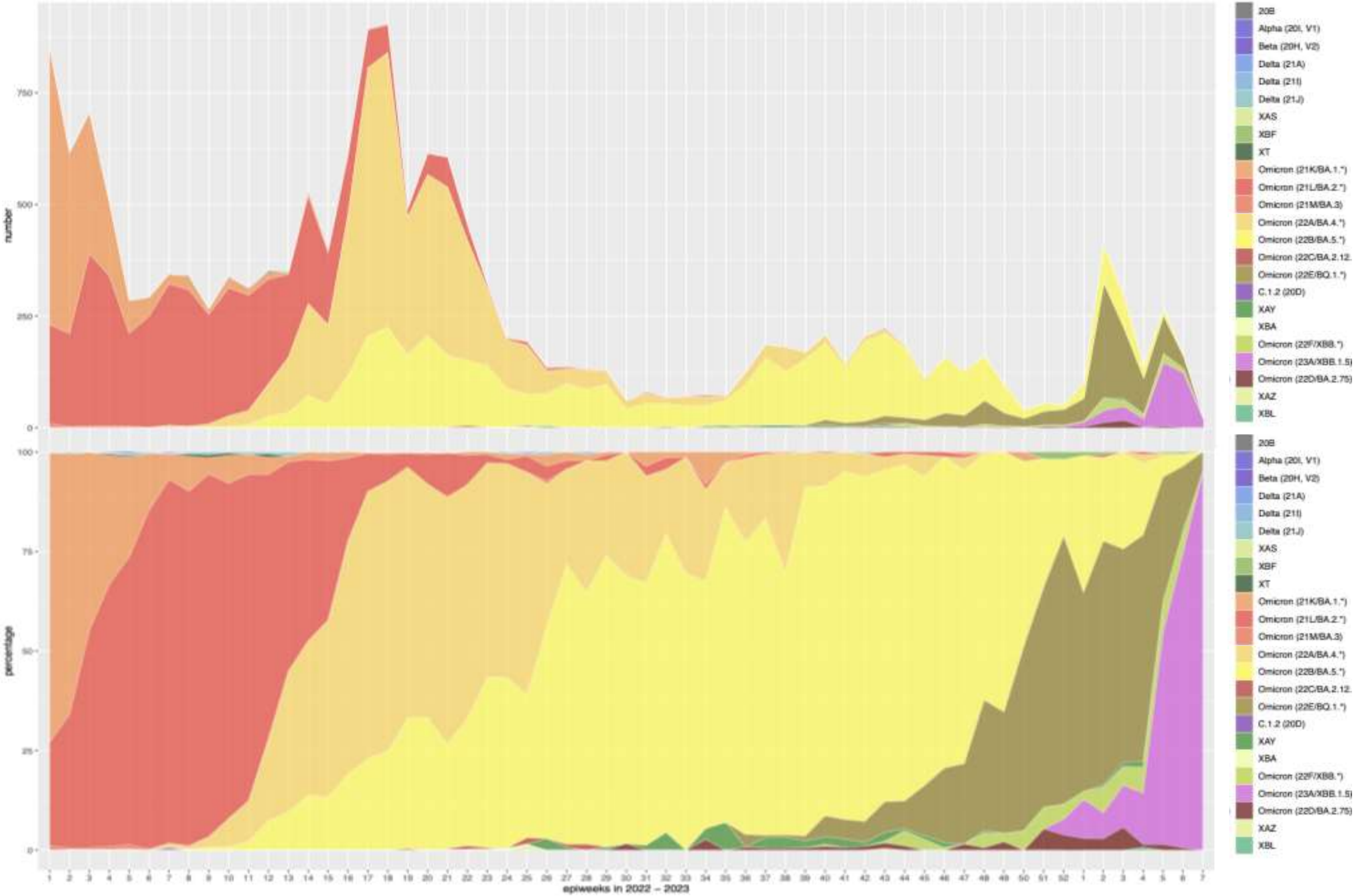
# Number and percentage of clades by epiweek in South Africa, 2022-2023 (16 716*)



Sequencing data ending epi week 7 (ending 18 Feb 2023)

Currently in epi week 9 (ending 05 Mar 2023)

*Excludes sequences missing collection dates, as well as those collected January 1st and 2nd 2021 as they are part of epiweek 53 of 2020.

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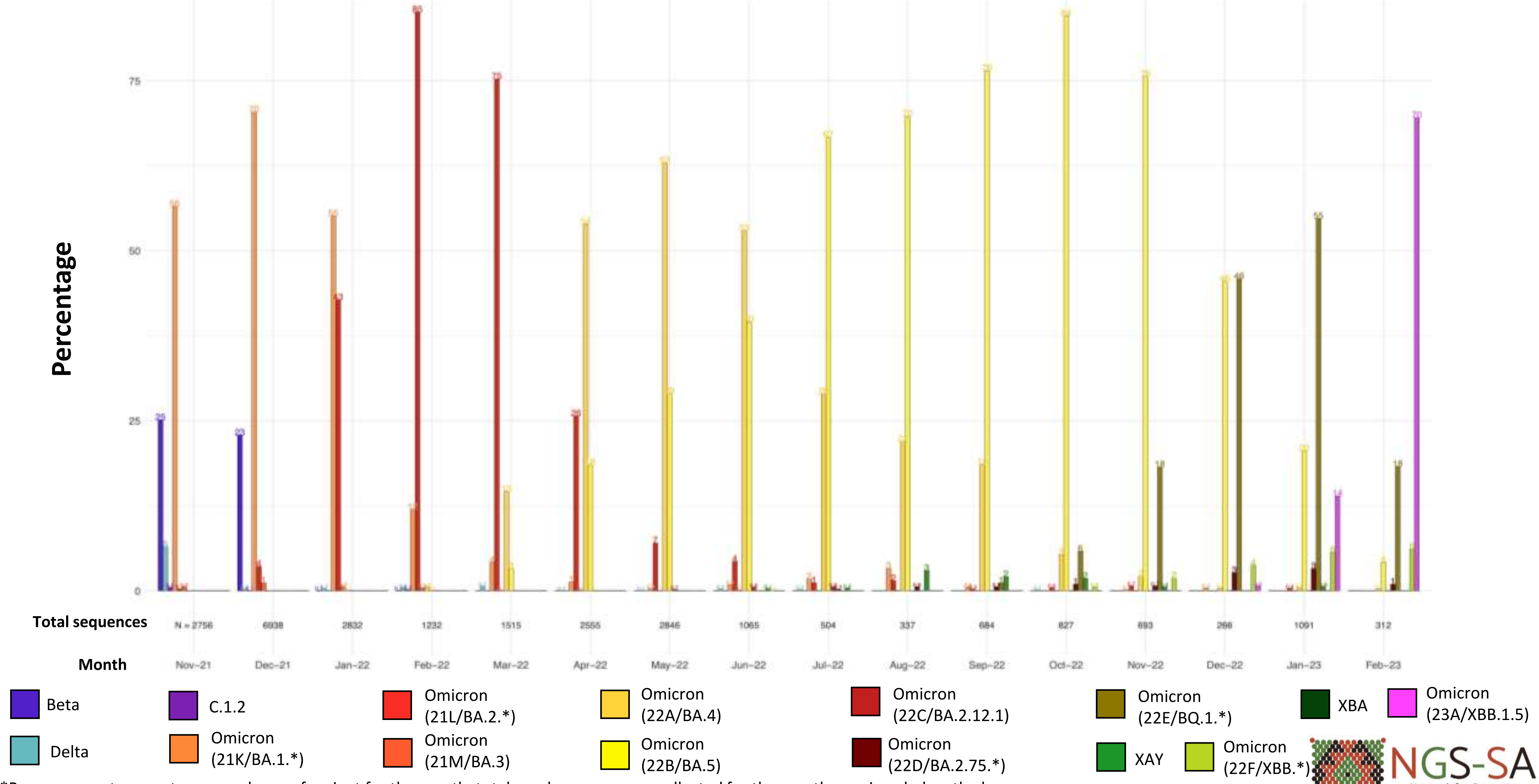
# Detection Rates: Beta, Delta, C.1.2, recombinants, and Omicron



*Bars represent percentage prevalence of variant for the month; total number sequences collected for the month are given below the bar

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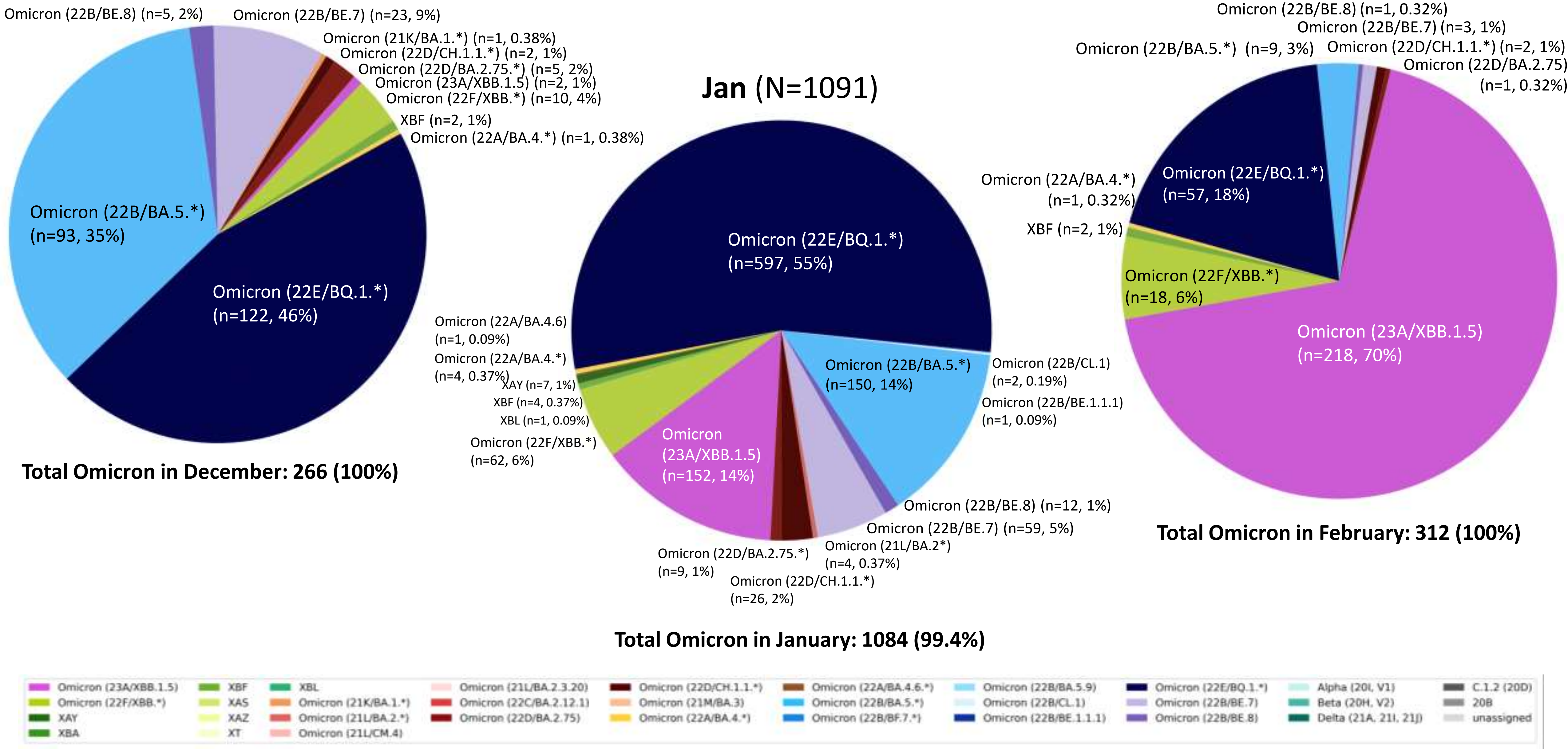
# Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in Dec 2022– Feb 2023

**Dec** (N=266)

**Jan** (N=1091)

**Feb** (N=312)



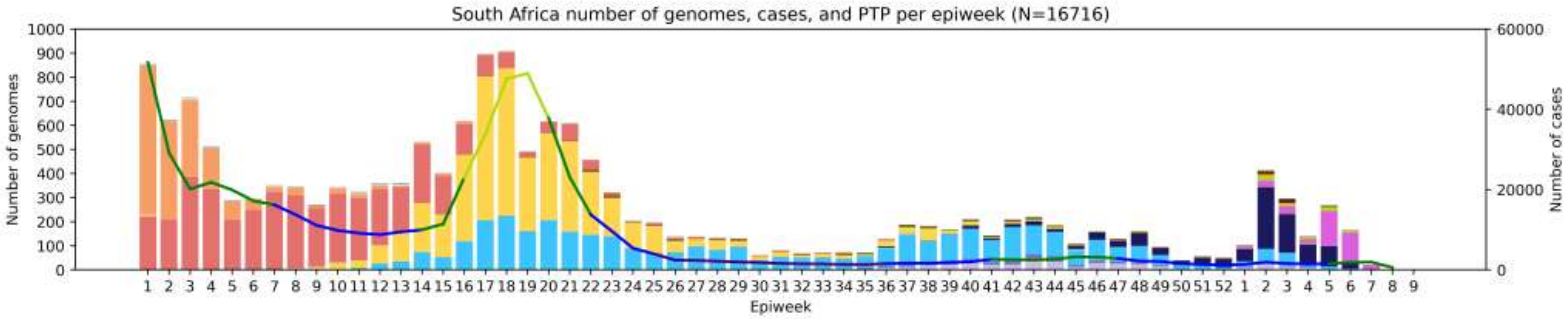
**Total Omicron in December: 266 (100%)**

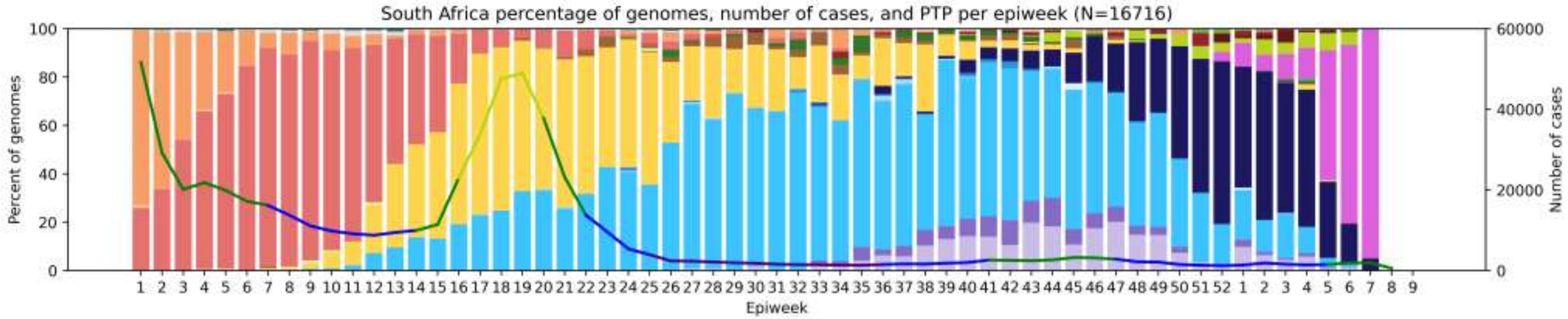
**Total Omicron in January: 1084 (99.4%)**

**Total Omicron in February: 312 (100%)**

Note: XBF and XBL are Omicron-Omicron recombinants and so are counted in the total number of Omicrons.

# South Africa, 2022-2023, n = 16 716*


South Africa number of genomes, cases, and PTP per epiweek (N=16716)


South Africa percentage of genomes, number of cases, and PTP per epiweek (N=16716)

Clade key (bar graph)

- Omicron (23A/XBB.1.5)
- Omicron (22F/XBB.*)
- XAY
- XBA
- XBF
- XAS
- XAZ
- XT
- XBL
- Omicron (21K/BA.1.*)
- Omicron (21L/BA.2.*)
- Omicron (21L/CM.4)
- Omicron (21L/BA.2.3.20)
- Omicron (22C/BA.2.12.1)
- Omicron (22D/BA.2.75)
- Cases
- Omicron (22D/CH.1.1.*)
- Omicron (21M/BA.3)
- Omicron (22A/BA.4.*)
- Omicron (22A/BA.4.6.*)
- Omicron (22B/BA.5.*)
- Omicron (22B/BF.7.*)
- Omicron (22B/BA.5.9)
- Omicron (22B/CL.1)
- Omicron (22B/BE.1.1.1)
- Omicron (22E/BQ.1.*)
- Omicron (22B/BE.7)
- Omicron (22B/BE.8)
- Alpha (20I, V1)
- Beta (20H, V2)
- Delta (21A, 21I, 21J)
- C.1.2 (20D)
- 20B
- unassigned

Weekly percentage testing positive key (line graph)

- ≤ 5
- 6 - 10
- 11 - 20
- 21 - 30
- 31 - 40
- 41 - 50
- 51 - 55

*Excludes sequences missing collection dates. Lineages of particular interest (mainly WHO Omicron subvariants under monitoring) are separate from the main clade groupings.

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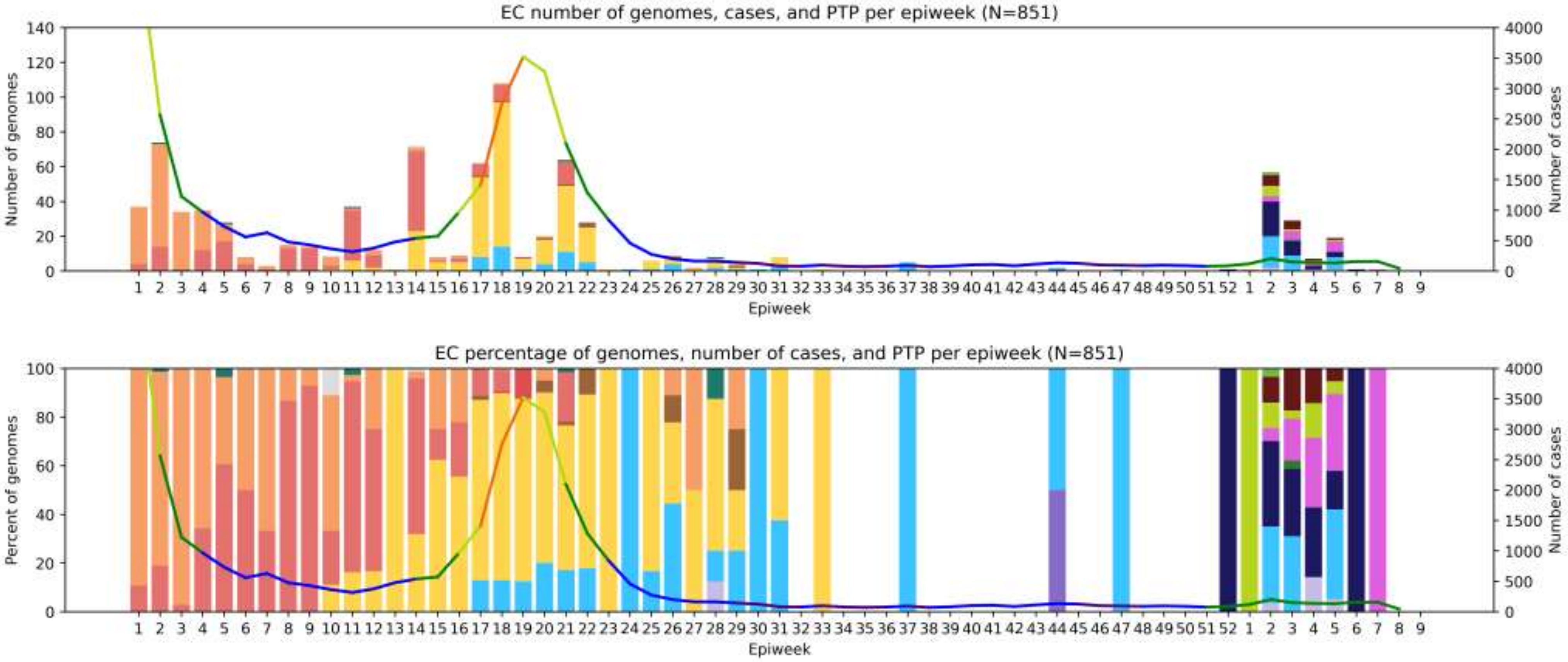
# Eastern Cape Province, 2022-2023, n = 851

Genomes added since last report: 0*



Clade key (bar graph)

- ■ Omicron (23A/XBB.1.5)
- ■ Omicron (22F/XBB.*)
- ■ XAY
- ■ XBA
- ■ XBF
- ■ XAS
- ■ XAZ
- ■ XT
- ■ XBL
- ■ Omicron (21K/BA.1.*)
- ■ Omicron (21L/BA.2.*)
- ■ Omicron (21L/CM.4)
- ■ Omicron (21L/BA.2.3.20)
- ■ Omicron (22C/BA.2.12.1)
- ■ Omicron (22D/BA.2.75)
- — Cases
- ■ Omicron (22D/CH.1.1.*)
- ■ Omicron (21M/BA.3)
- ■ Omicron (22A/BA.4.*)
- ■ Omicron (22A/BA.4.6.*)
- ■ Omicron (22B/BA.5.*)
- ■ Omicron (22B/BF.7.*)
- ■ Omicron (22B/BA.5.9)
- ■ Omicron (22B/CL.1)
- ■ Omicron (22B/BE.1.1.1)
- ■ Omicron (22E/BQ.1.*)
- ■ Omicron (22B/BE.7)
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- ■ Alpha (20I, V1)
- ■ Beta (20H, V2)
- ■ Delta (21A, 21I, 21J)
- ■ C.1.2 (20D)
- ■ 20B
- ■ unassigned

Weekly percentage testing positive key (line graph)

— ≤ 5 — 6 - 10 — 11 - 20 — 21 - 30 — 31 - 40 — 41 - 50 — 51 - 55

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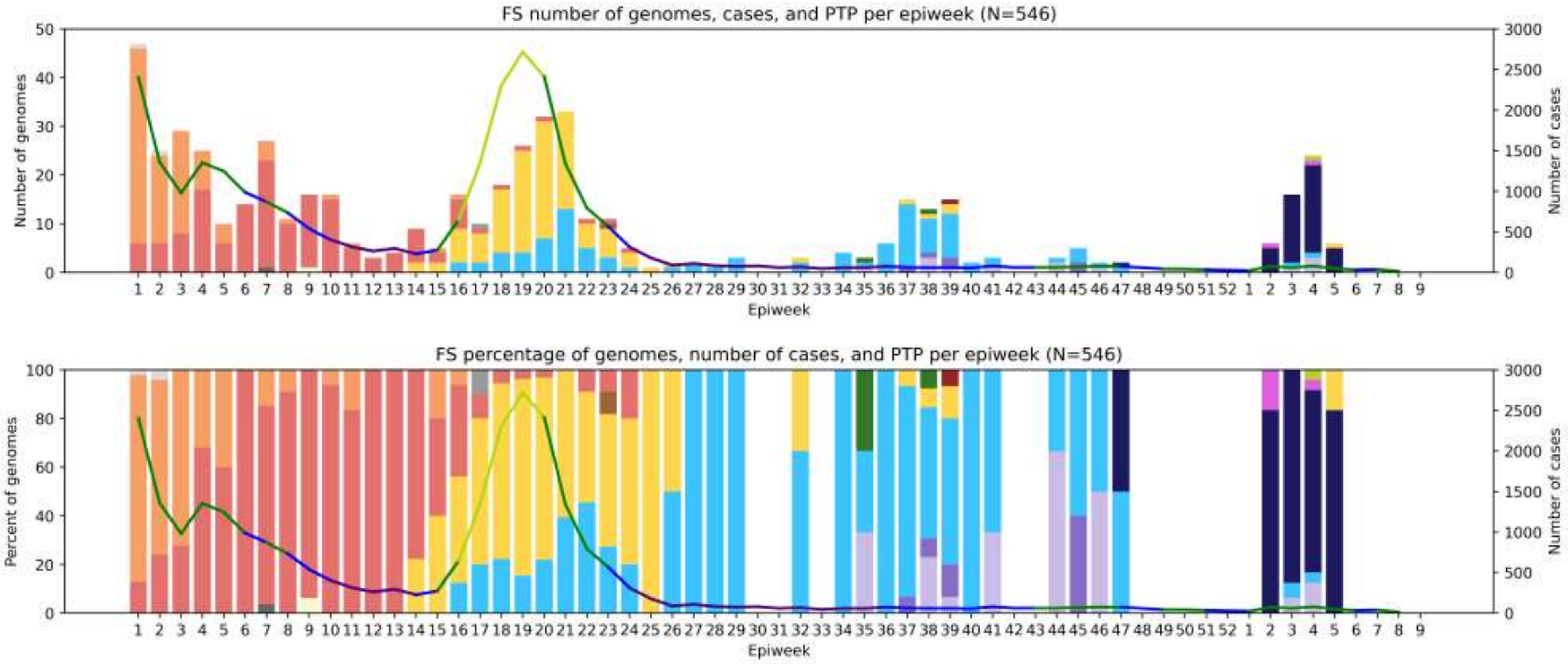
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

# Free State Province, 2022-2023, n = 546

Genomes added since last report: 0*



Clade key (bar graph)

- ■ Omicron (23A/XBB.1.5)
- ■ Omicron (22F/XBB.*)
- ■ XAY
- ■ XBA
- ■ XBF
- ■ XAS
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- ■ Omicron (21K/BA.1.*)
- ■ Omicron (21L/BA.2.*)
- ■ Omicron (21L/CM.4)
- ■ Omicron (21L/BA.2.3.20)
- ■ Omicron (22C/BA.2.12.1)
- ■ Omicron (22D/BA.2.75)
- — Cases
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Weekly percentage testing positive key (line graph)

— ≤ 5 — 6 - 10 — 11 - 20 — 21 - 30 — 31 - 40 — 41 - 50 — 51 - 55

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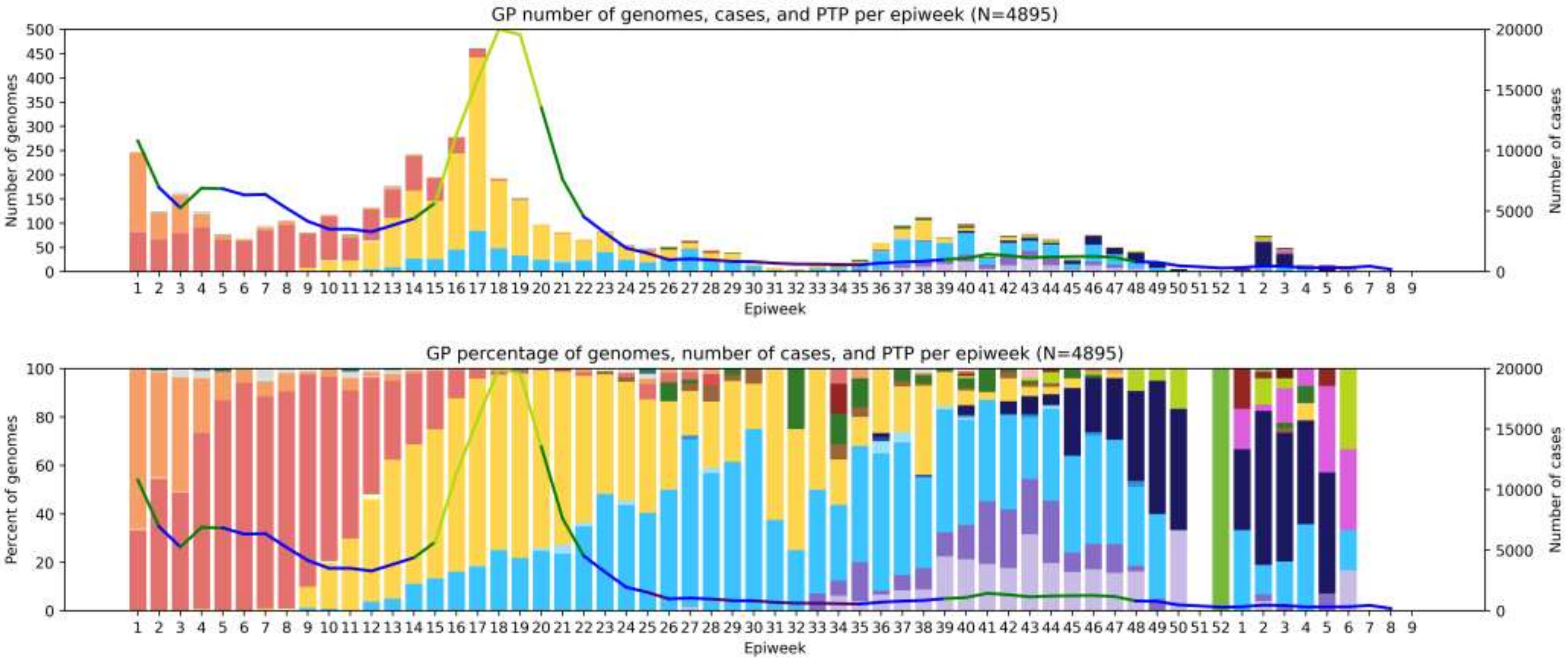
# Gauteng Province, 2022-2023, n = 4895

Genomes added since last report: 0*



Clade key (bar graph)

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■ Omicron (22A/BA.4.*)
■ Omicron (22A/BA.4.6.*)
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■ Omicron (22B/BF.7.*)
■ Omicron (22B/BA.5.9)
■ Omicron (22B/CL.1)
■ Omicron (22B/BE.1.1.1)
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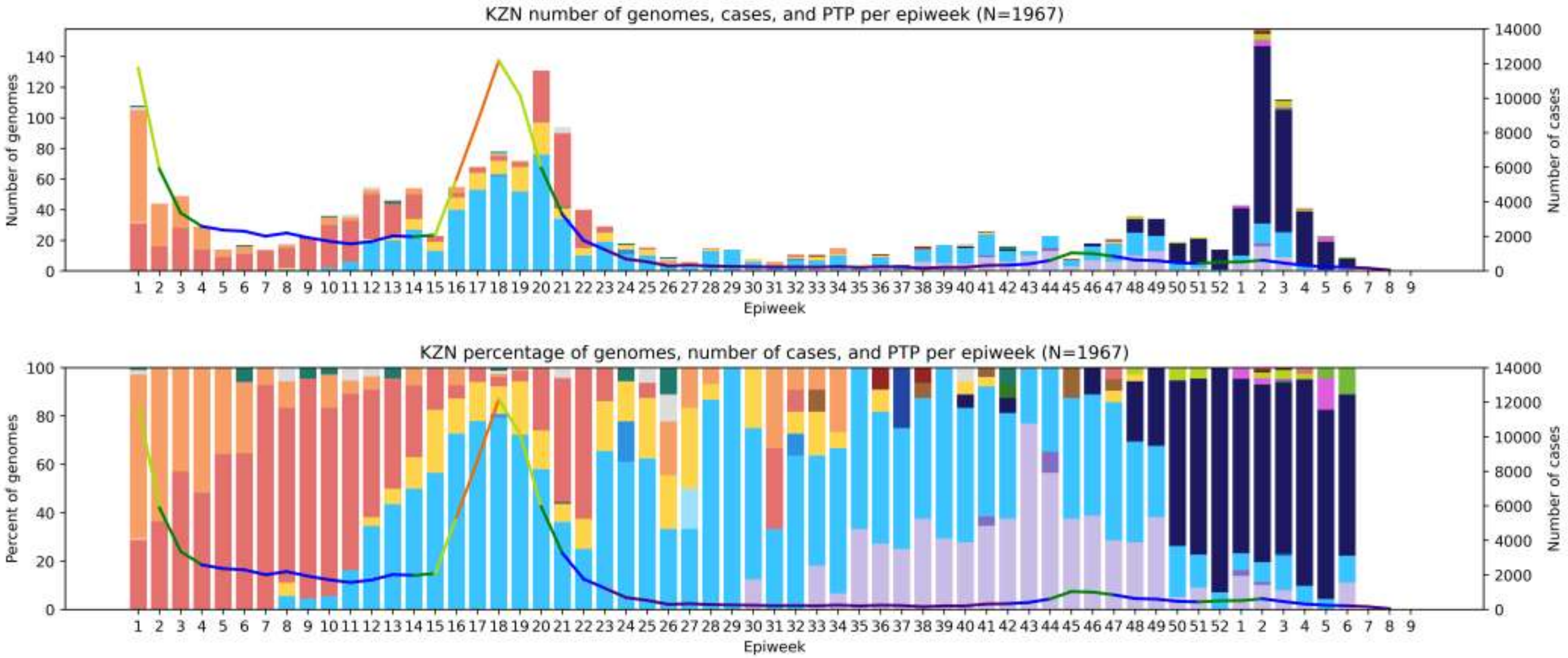
# KwaZulu-Natal Province, 2022-2023, n = 1967

Genomes added since last report: 0*



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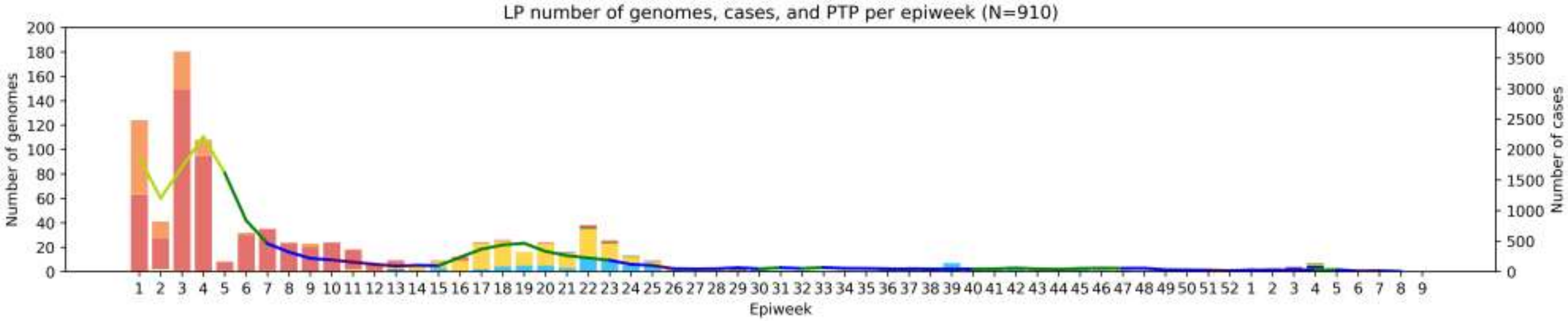
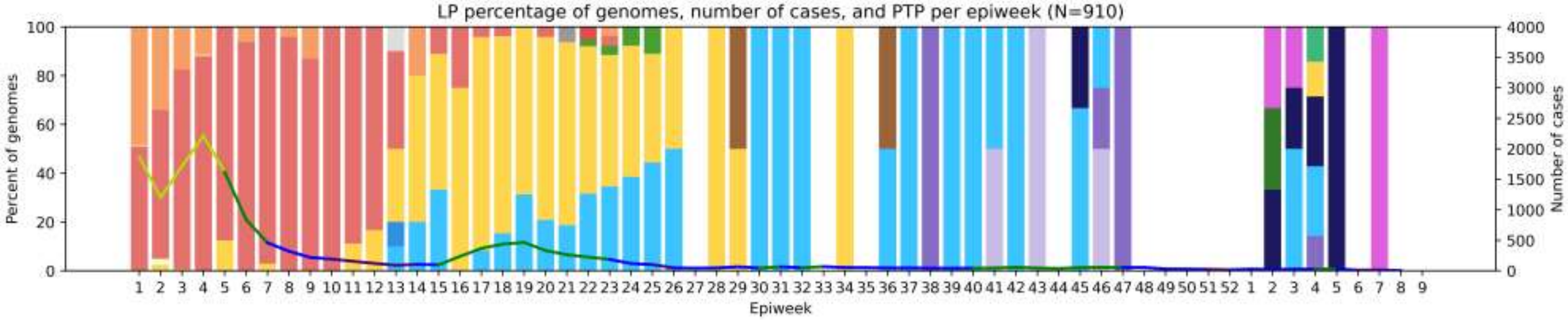
# Limpopo Province, 2022-2023, n = 910

Genomes added since last report: 0*





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Weekly percentage testing positive key (line graph)

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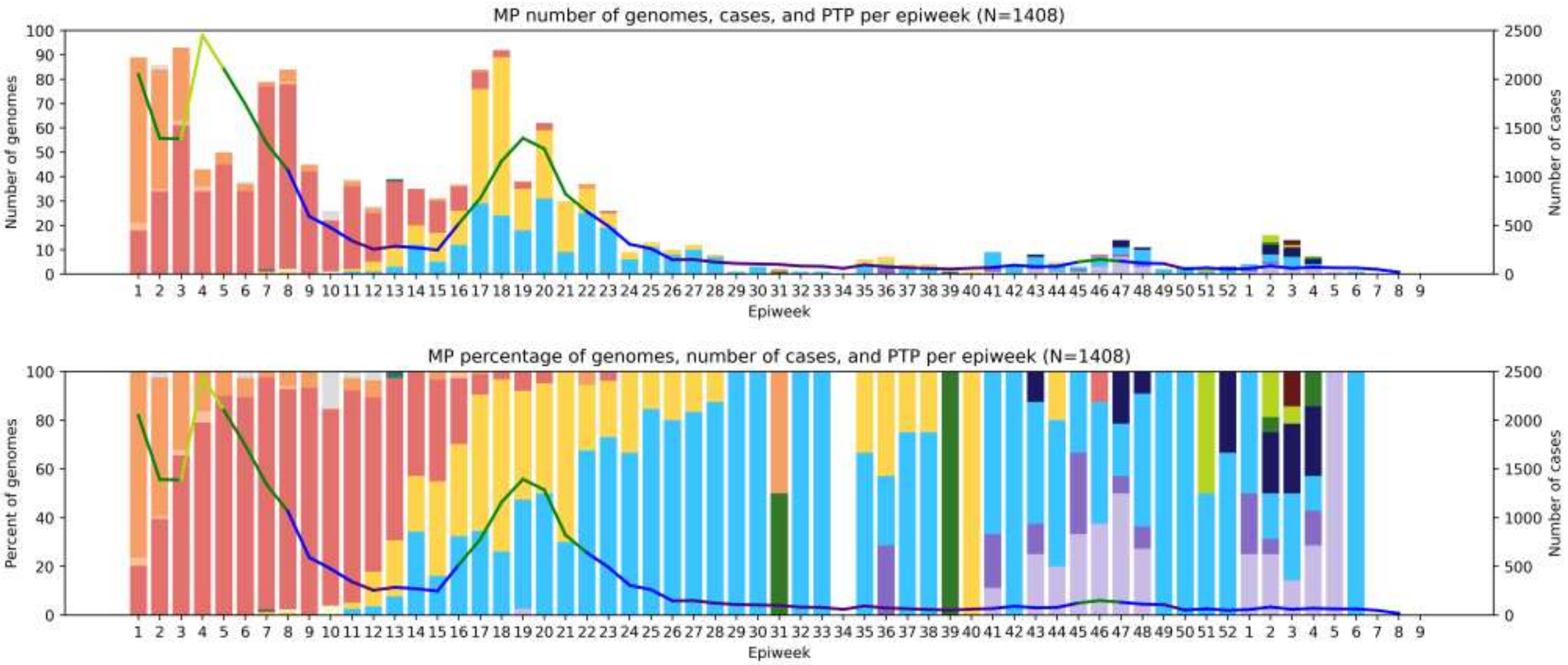
# Mpumalanga Province, 2022-2023, n = 1408

Genomes added since last report: 0*



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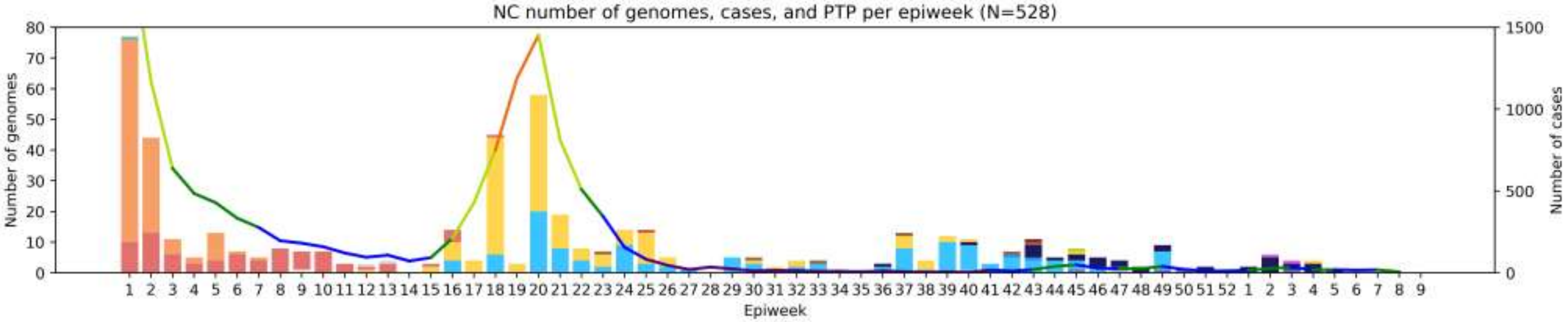
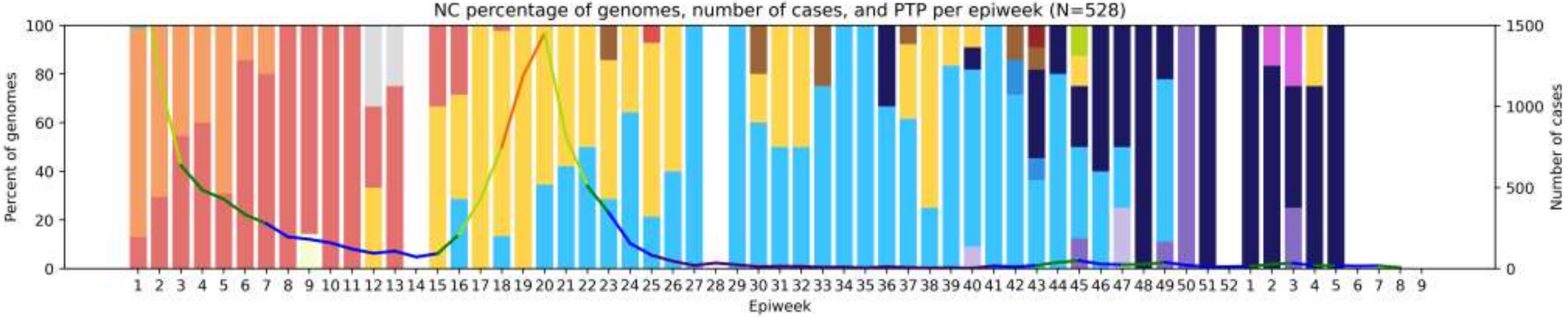
# Northern Cape Province, 2022-2023, n = 528

Genomes added since last report: 15*





Clade key (bar graph)

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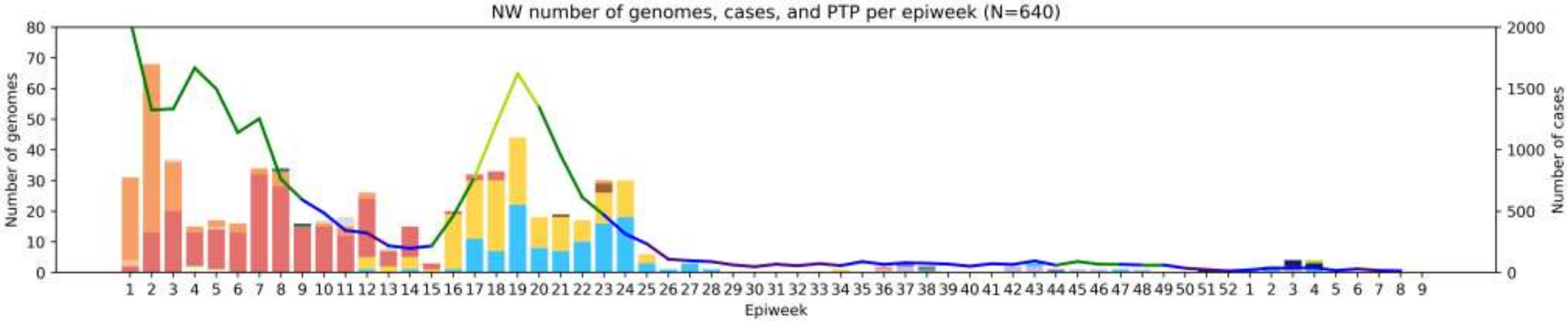
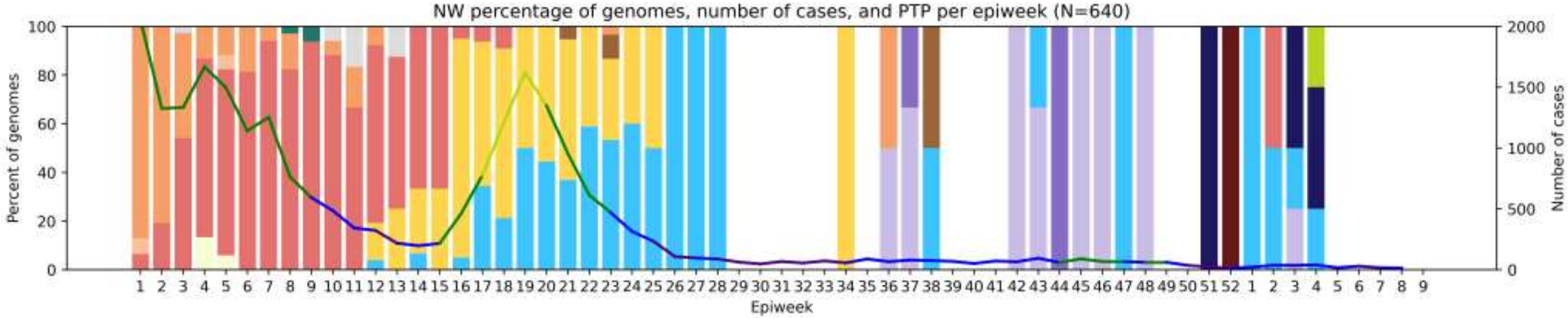
# North West Province, 2022-2023, n = 640

Genomes added since last report: 0*





Clade key (bar graph)

- Omicron (23A/XBB.1.5)
- Omicron (22F/XBB.*)
- XAY
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- Omicron (21M/BA.3)
- Omicron (22A/BA.4.*)
- Omicron (22A/BA.4.6.*)
- Omicron (22B/BA.5.*)
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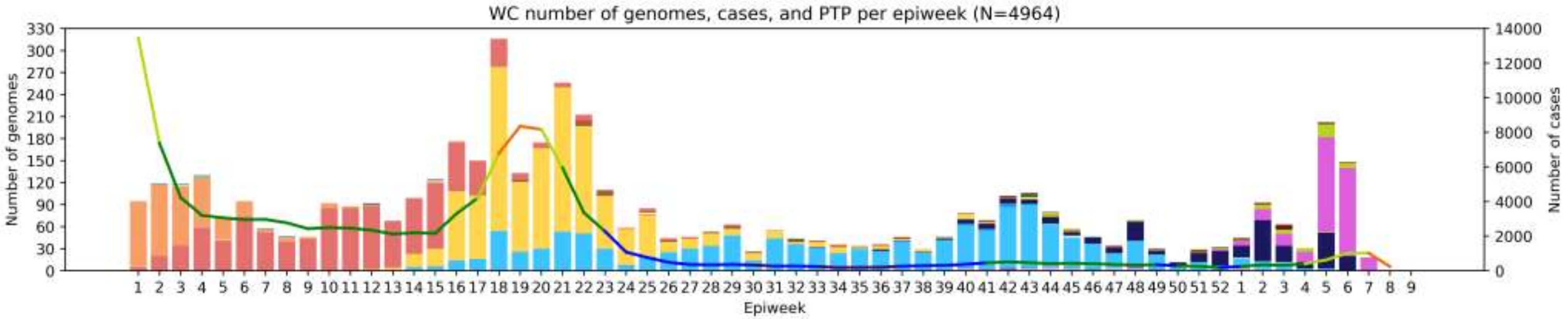
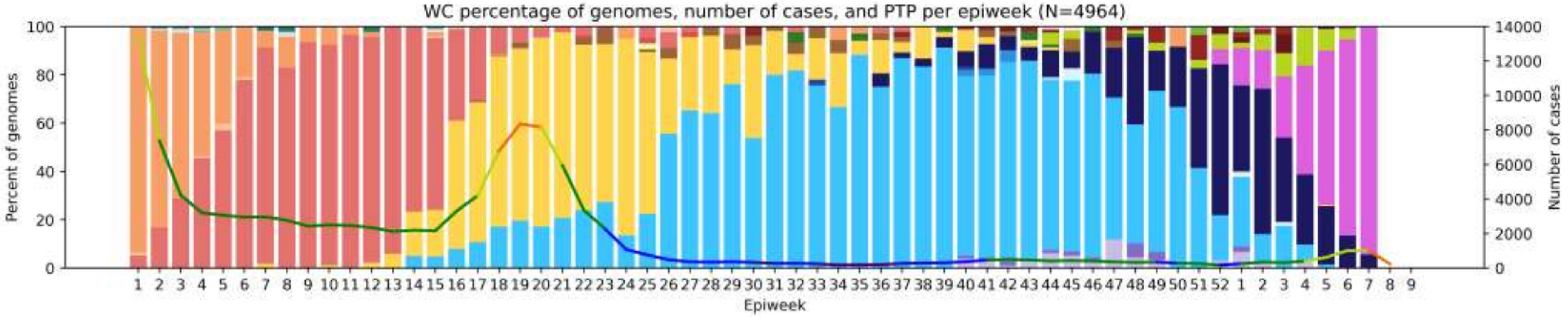
# Western Cape Province, 2022-2023, n = 4964

Genomes added since last report: 30*


WC number of genomes, cases, and PTP per epiweek (N=4964)


WC percentage of genomes, number of cases, and PTP per epiweek (N=4964)

Clade key (bar graph)

- ▬ Omicron (23A/XBB.1.5)
- ▬ Omicron (22F/XBB.*)
- ▬ XAY
- ▬ XBA
- ▬ XBF
- ▬ XAS
- ▬ XAZ
- ▬ XT
- ▬ XBL
- ▬ Omicron (21K/BA.1.*)
- ▬ Omicron (21L/BA.2.*)
- ▬ Omicron (21L/CM.4)
- ▬ Omicron (21L/BA.2.3.20)
- ▬ Omicron (22C/BA.2.12.1)
- ▬ Omicron (22D/BA.2.75)
- — Cases
- ▬ Omicron (22D/CH.1.1.*)
- ▬ Omicron (21M/BA.3)
- ▬ Omicron (22A/BA.4.*)
- ▬ Omicron (22A/BA.4.6.*)
- ▬ Omicron (22B/BA.5.*)
- ▬ Omicron (22B/BF.7.*)
- ▬ Omicron (22B/BA.5.9)
- ▬ Omicron (22B/CL.1)
- ▬ Omicron (22B/BE.1.1.1)
- ▬ Omicron (22E/BQ.1.*)
- ▬ Omicron (22B/BE.7)
- ▬ Omicron (22B/BE.8)
- ▬ Alpha (20I, V1)
- ▬ Beta (20H, V2)
- ▬ Delta (21A, 21I, 21J)
- ▬ C.1.2 (20D)
- ▬ 20B
- ▬ unassigned

Weekly percentage testing positive key (line graph)

- — ≤ 5
- — 6 - 10
- — 11 - 20
- — 21 - 30
- — 31 - 40
- — 41 - 50
- — 51 - 55

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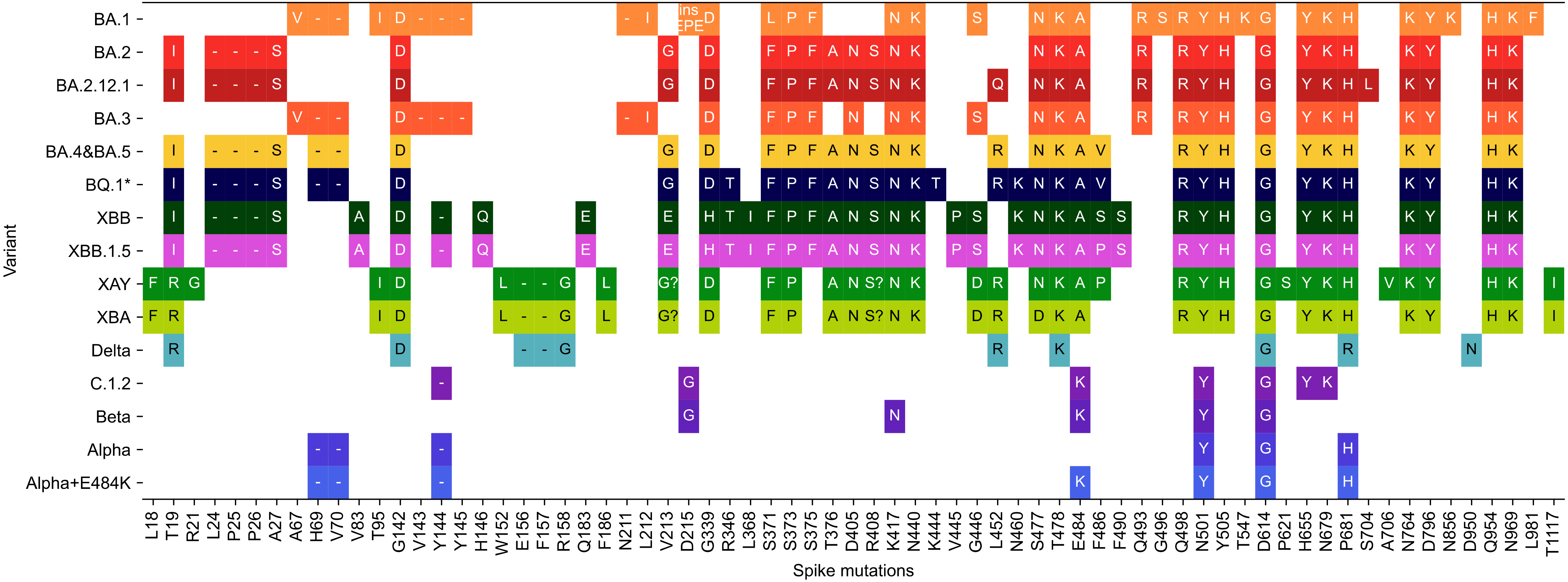
*May include genomes from 2020 and 2021 which are not pictured here and are not included in the slide total.

# Summary

- **Sequencing update**
  - Eastern Cape, Gauteng, KwaZulu-Natal, Mpumalanga, the Northern Cape, the North West and the Western Cape have sequences for December 2022. All provinces have sequences for January 2023. All provinces, except the North West, have sequences for February 2023

- **Variant of Concern Omicron in South Africa**
  - Omicron continued to dominate in December (100%), January (99%) and makes up 100% of February sequences
  - BQ.1 and sub-lineages were the dominant Omicron lineage in December (46%) and January (55%).
  - XBB.1.5 was detected in December 2022 (n=2, 1%) and January 2023 (n=152, 14%), and is the dominant lineage in February 2023 (n=218, 70%)
  - BA.2.75.* continued to be detected at a low prevalence in December, January and February (≤3%)

# Spike protein mutation* profile of Variants of Interest and Concern



- Multiple changes within the two immunogenic regions in S1 (NTD and RBD)
  - Including a three amino acid insertion
- Accumulation of mutations surrounding the furin cleavage site
  - Including combination of N679K and P681H
- Effect of most spike S2 subunit changes have not been defined, but may be linked to immune escape

*Only mutations present in Omicron, Delta, or recombinant sequences are pictured

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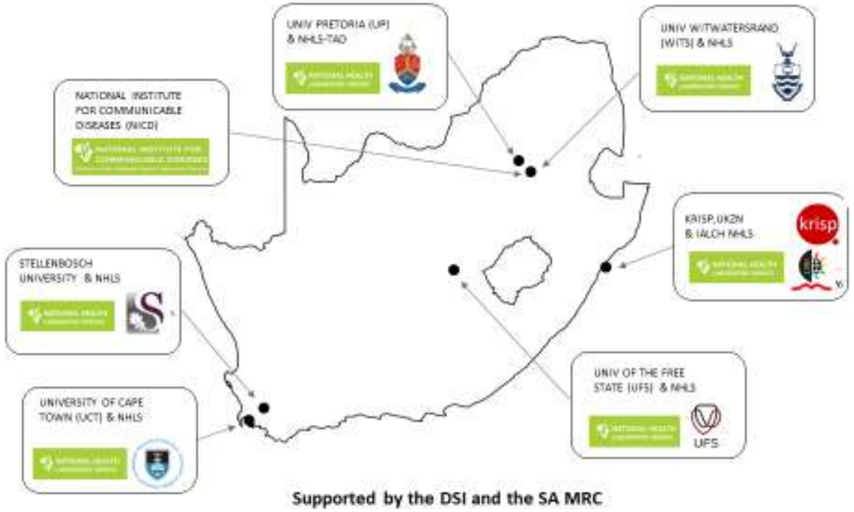

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UNIVERSITY OF PRETORIA
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STELLENBOSCH
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science & innovation
Department:
Science and Innovation
REPUBLIC OF SOUTH AFRICA

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Division of the National Health Laboratory Service

EDCTP

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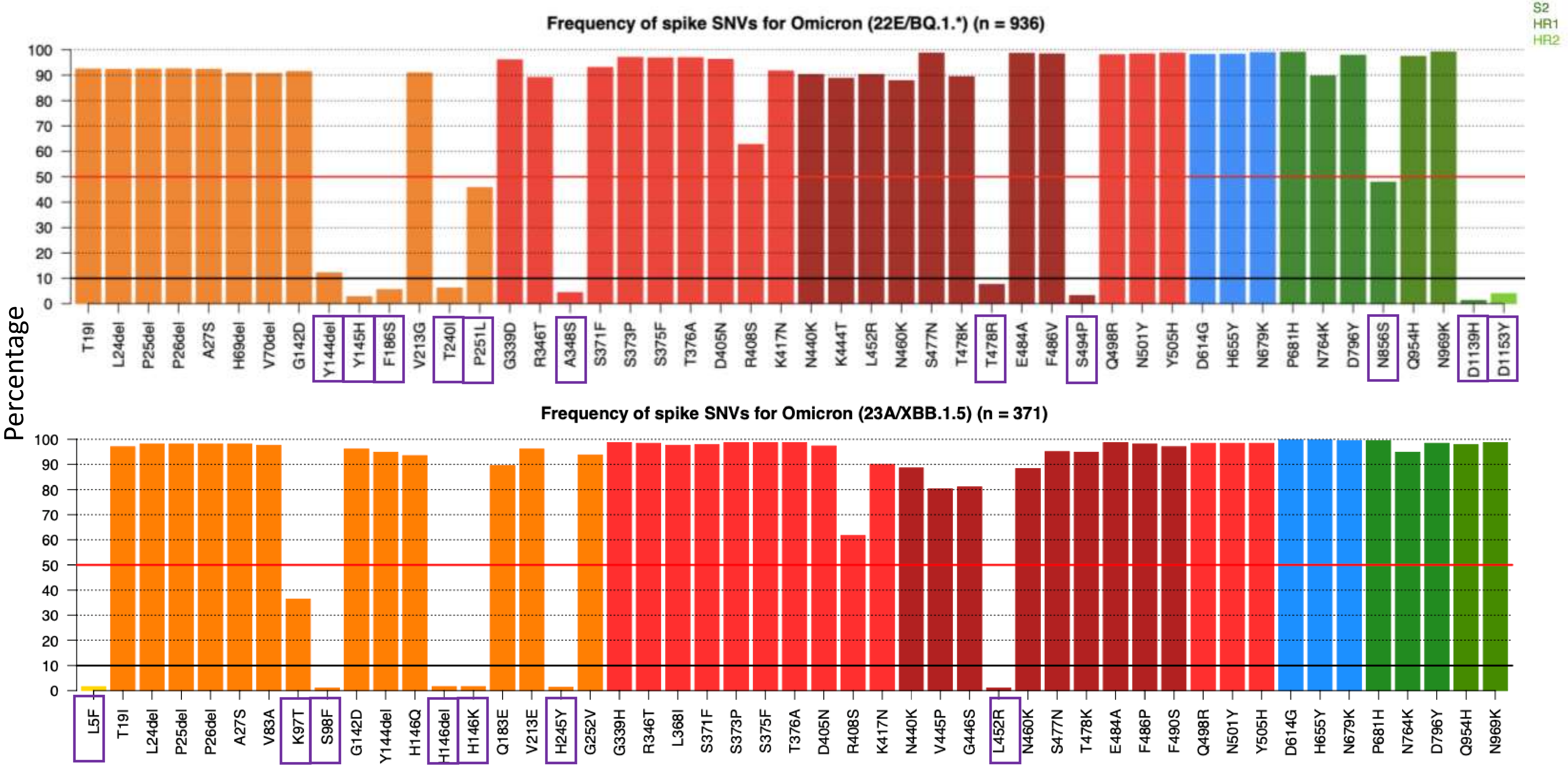
# BQ.1* and XBB.1.5* spike mutations*



*Only mutations present in ≥1% of sequences are shown.

## University of Stellenbosch & NHLS Tygerberg Virology

Susan Engelbrecht
Wolfgang Preiser
Gert van Zyl
Tongai Maponga
Bronwyn Kleinhans
Shannon Wilson
Karabo Phadu
Tania Stander
Kamela Mahlakwane
Mathilda Claassen
Diagnostic laboratory staff

## UKZN-Inkosi Albert Luthuli Central Hospital

Dr Khanyi Msomi
Dr Kerusha Govender
Dr Pravi Moodley
Dr Aabida Khan
Dr Lili Gounder
Dr Kerri Francois
Dr Cherise Naicker
Dr Joedene Chetty

Dr Neli Ngcaba
Dr Tshepiso Mosito
Mr Malcolm Ellapen
Mr Kubendran Reddy
The COVID-19 Bench team

## University of KwaZulu-Natal & Africa Health Research Institute

**KRISP at UKZN:**
Tulio de Oliveira
Richard Lessels
Houriiyah Tegally
Eduan Wilkinson
Jennifer Giandhari
Sureshnee Pillay
Emmanuel James San

**AHRI**
Alex Sigal
Sandile Cele
Willem Hanekom

## University of Cape Town, NHLS & Western Cape Government

**NHLS-UCT**
Carolyn Williamson
Nei-yuan Hsiao
Diana Hardie
Kruger Marais
Stephen Korsman
Ziyaad Valley-Omar

**WCG-UCT**
Mary-Anne Davies
Hannah Hussey
Andrew Boulle
Masudah Paleker
Theuns Jacobs
Erna Morden

**NHLS Greenpoint**
Annabel Enoch

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**UCT, IDM and CIDRI-Africa**
Deelan Doolabh
Arash Iranzadeh
Lynn Tyers
Innocent Mudau
Nokuzola Mbhele
Fezokuhle Khumalo
Thabang Serakge
Bruna Galvão
Arghavan Alisoltani (U. California)

Robert Wilkinson
Darren Martin
Nicola Mulder
Wendy Burgers
Ntobeko Ntusi
Rageema Joseph
Sean Wasserman
Linda Boloko

## Zoonotic arbo and respiratory virus program
## Centre for Viral Zoonoses
## Department Medical Virology/ NHLS Tshwane Academic division
## University of Pretoria

**ZARV research program/UP**
Marietjie Venter (Head: ZARV)
Adriano Mendes (Postdoc)
Amy Strydom (Postdoc)
Michaela Davis (MSc, intern medical scientist)
Carien van Niekerk

**NHLS Tshwane**
Prof Simnikiwe Mayaphi (HOD)

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## National Institute for Communicable Diseases

**Centre for Respiratory Diseases & Meningitis**
Anne von Gottberg
Thabo Mohale
Daniel Amoako
Josie Everatt
Boitshoko Mahlangu
Noxolo Ntuli
Anele Mnguni
Amelia Buys
Cardia Fourie
Noluthando Duma
Linda de Gouveia
Jackie Kleynhans
Nicole Wolter
Sibongile Walaza
Mignon du Plessis
Stefano Tempia
Mvuyo Makhasi
Cheryl Cohen

**Centre for HIV and STIs**
Jinal Bhiman
Cathrine Scheepers
Constantinos Kurt Wibmer
Thandeka Moyo
Tandile Hermanus
Frances Ayres
Zanele Molaudzi
Bronwen Lambson
Tandile Hermanus
Mashudu Madzivhandila
Prudence Kgagudi
Brent Oosthuysen
Penny Moore
Lynn Morris

**NICD Groups**
NICD COVID-19 response team
NICD SARS-CoV-2 Sequencing Group

**Sequencing Core Facility**
Zamantungwa Khumalo
Annie Chan
Morne du Plessis
Stanford Kwenda
Phillip Senzo Mtshali
Mushal Allam
Florah Mnyameni
Arshad Ismail

## University of the Free State

**UFS**
Dominique Goedhals
Armand Bester
Martin Myaga
Peter Mwangi
Emmanuel Ogunbayo
Milton Mogotsi
Makgotso Maotoana
Lutfiyya Mohamed

**NHLS Division of Virology**
Sabeehah Vawda
Felicity Burt
Thokozani Mkhize
Diagnostic laboratory staff

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# Additional support and collaborators

**NHLS**
Koeleka Mlisana
Zinhle Makatini
Eugene Elliot
Florette K. Treurnicht
Kathleen Subramoney
Oluwakemi Laguda-Akingba
Shareef Abrahams
Greta Hoyland
Gloria Selabe
Elias Bereda
Jeannette Wadula

**Hyrax Biosciences**
Simon Travers

**Cape Town HVTN Laboratory**
Erica Anderson-Nissen
Anneta Naidoo

**Ndlovu Research**
Hugo Tempelman
CJ Umunnakwe

**Lancet**
Allison J. Glass
Raquel Viana

**Ampath**
Terry Marshall
Cindy van Deventer
Eddie Silberbauer

**Pathcare Vermaak**
Andries Dreyer
Howard Newman
Riaan Writes
Marianne Wolfaardt
Warren Lowman

**Bridge-the-Gap**
Raymond Rott

**Cytespace Africa Laboratories**
Christa Viljoen

**ARC-OVI**
Lia Rotherham

**CAPRISA**
Salim Abdool Karim
Nigel Garret

**UKZN - Big Data**
Francesco Pettruccione
Ilya Sinayskiy

**University of Oxford**
José Lourenço

**FioCruz, Brazil**
Vagner Fonseca
Marta Giovanetti
Luiz Carlos Junior Alcantara

**Africa CDC and Africa PGI**
John Nkengasong
Sofonias Tessema

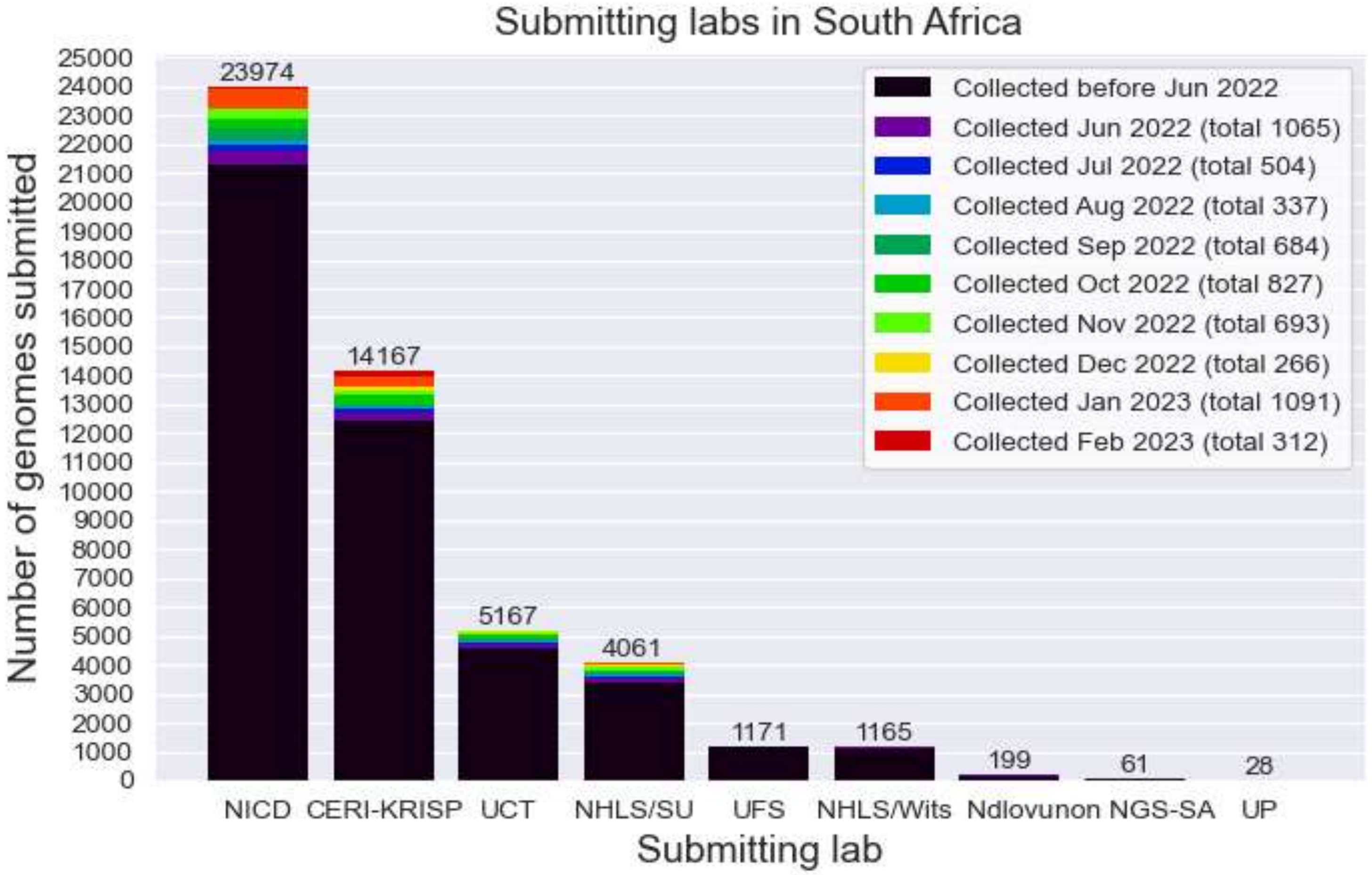
**Netcare**
Richard Friedland
Craig Murphy
Caroline Maslo
Liza Sitharam

**DSI**
Glaudina Loots

**SA MRC**
Glenda Gray

**Pathcare N1 City**
Jean Maritz
Nadine Cronje
Petra Raimond
Kim Hoek

# South African genomes submitted per submitting lab, 2020 - 2023 (N=49 993)



**NGS-SA Labs**

**CERI**: Centre for Epidemic Response and Innovation

**KRISP**: KZN Research Innovation and Sequencing Platform

**NDLOVU:** Ndlovu Research Laboratories

**NICD**: National Institute for Communicable Diseases

**NHLS**: National Health Laboratory Service

**SU**: Stellenbosch University

**UCT**: University of Cape Town

**UFS**: University of the Free State

**UP**: University of Pretoria

**Multiple labs from NGS-SA and collaborating public and private laboratories are contributing to sequencing, both as originating and as submitting (pictured here) laboratories.**

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# Currently circulating Variants of Concern (VOC)

| WHO label | Pango lineage• | GISAID clade | Nextstrain clade | Additional amino acid changes monitored° | Earliest documented samples | Date of designation |
|---|---|---|---|---|---|---|
| Omicron* | B.1.1.529 | GR/484A | 21K, 21L, 21M, 22A, 22B, 22C, 22D | +S:R346K<br>+S:L452X<br>+S:F486V | Multiple countries, Nov-2021 | VUM: 24-Nov-2021<br>VOC: 26-Nov-2021 |

* Includes BA.1, BA.2, BA.3, BA.4, BA.5 and descendent lineages. It also includes BA.1/BA.2 circulating recombinant forms such as XE. WHO emphasizes that these descendant lineages should be monitored as distinct lineages by public health authorities and comparative assessments of their virus characteristics should be undertaken.

° Only found in a subset of sequences

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 24 February 2023

# Omicron subvariants under monitoring

| Pango lineage[#] (+ mutation) | GISAID clade | Nextstrain clade | Relationship to circulating VOC lineages | Spike genetic features | Earliest documented samples |
|---|---|---|---|---|---|
| BF.7* | GRA | 22B | BA.5 sublineage | BA.5 + S:R346T | 24-01-2022 |
| BQ.1[$] | GRA | 22E | BA.5 sublineage | BQ.1 and BQ.1.1: BA.5 + S:R346T, S:K444T, S:N460K | 07-02-2022 |
| BA.2.75[§] | GRA | 22D | BA.2 sublineage | BA.2.75: BA.2 + S:K147E, S:W152R, S:F157L, S:I210V, S:G257S, S:D339H, S:G446S, S:N460K, S:Q493R reversion | 31-12-2021 |
| CH.1.1[§] | GRA | 22D | BA.2 sublineage | BA.2.75 + S:L452R, S:F486S | 27-07-2022 |
| XBB[µ] | GRA | 22F | Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1, with a breakpoint in S1 | BA.2+ S:V83A, S:Y144-, S:H146Q, S:Q183E, S:V213E, S:G252V, S:G339H, S:R346T, S:L368I, S:V445P, S:G446S, S:N460K, S:F486S, S:F490S | 13-08-2022 |
| XBB.1.5 | GRA | 23A | Recombinant of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1, with a breakpoint in S1 | XBB + S:F486P (see rapid risk assessment) | 05-01-2022 |
| XBF | GRA |  | Recombinant of BA.5.2.3 and CJ.1 (BA.2.75.3 sublineage) | BA.5 + S:K147E, S:W152R, S:F157L, S:I210V, S:G257S, S:G339H, S:R346T, S:G446S, S:N460K, S:F486P, S:F490S | 27-07-2022 |

[#] includes descendent lineages

[*] additional mutations outside of the spike protein: N: G30-, S33F, ORF9b: M26-, A29I, V30L

[$] additional mutation outside the spike protein: ORF1a: Q556K, L3829F, ORF1b: Y264H, M1156I, N1191S, N: E136D, ORF9b: P10F

[§] additional mutations outside of the spike protein: ORF1a: S1221L, P1640S, N4060S, ORF1b: G662S, E: T11A

[µ] additional mutations outside of the spike protein: ORF1a: K47R, ORF1b: G662S, S959P, E: T11A, ORF8: G8*

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 24 February 2023

# Previously circulating Variants of Concern

| WHO label | Pango lineage• | GISAID clade | Nextstrain clade | Earliest documented samples | Date of designation |
|---|---|---|---|---|---|
| Alpha | B.1.1.7 | GRY | 20I (V1) | United Kingdom, Sep-2020 | VOC: 18-Dec-2020<br>Previous VOC: 09-Mar-2022 |
| Beta | B.1.351 | GH/501Y.V2 | 20H (V2) | South Africa, May-2020 | VOC: 18-Dec-2020<br>Previous VOC: 09-Mar-2022 |
| Gamma | P.1 | GR/501Y.V3 | 20J (V3) | Brazil, Nov-2020 | VOC: 11-Jan-2021<br>Previous VOC: 09-Mar-2022 |
| Delta | B.1.617.2 | G/478K.V1 | 21A, 21I, 21J | India, Oct-2020 | VOI: 4-Apr-2021<br>VOC: 11-May-2021<br>Previous VOC: 7-Jun-2022 |

• Includes all descendant lineages. See the cov-lineages.org and the Pango network websites for further details.

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ accessed 24 February 2023

# Submission of routine specimens for sequencing

- representative of multiple geographic regions (provinces/districts/health facilities) from individuals of
  - all ages
  - over as many time periods during the SARS-CoV-2 epidemic in South Africa
- requested that testing laboratories in both the private and public sectors, submit respiratory samples to their closest NGS-SA sequencing laboratory on a routine basis (ideally every week) as follows, depending on the capacity of the testing laboratory:
  - All positives samples should be sent every week (NGS-SA laboratory will perform random sampling as described below) **OR**
  - A weekly selection of approximately 10%-20% of randomly selected positive samples should be sent every week. Number of selected samples will depend on the size of laboratory and how many other laboratories are drained by the submitting laboratory.

# Submission of special interest specimens for sequencing

In addition to routine samples mentioned above, please send specimens separately to above and clearly marked if:

- Suspected vaccine breakthrough (≥14 days after vaccine), especially if hospitalised and clinically severe
- Suspected re-infection (≥90 days after previous episode), especially if hospitalised and clinically severe
- Prolonged shedding with high SARS-CoV-2 viral loads (i.e. Ct values less than 30 for more than 1 month post-primary diagnosis) in immunocompromised individuals
- Possible animal-to-human transmission
- Suspected cases of importation from another country, especially countries known to harbour SARS-CoV-2 variants of concern or countries with little available information
- Clusters of “unusual” cases (e.g., in terms of disease presentation, patient groups affected, etc.)